

whereby said DNA construct becomes integrated into a genome of said plant cell;

regenerating a plant from said transformed plant cell, and growing said plant under conditions whereby said DNA

5 sequence of interest is expressed and a plant having said regulatable phenotype is obtained.

2. A method for altering the phenotype of fruit tissue as distinct from other plant tissue, said method comprising:

10 growing a plant, wherein said plant comprises cells containing a DNA construct integrated into their genome, said DNA construct comprising, in the 5' to 3' direction of transcription, a transcriptional initiation region from a gene, wherein transcription of said gene is preferentially regulated in a plant fruit tissue, a DNA sequence of interest other than the coding sequence native to said
15 transcriptional initiation region, and a transcriptional termination region, whereby said DNA sequence of interest is transcribed under transcriptional control of said transcriptional initiation region and a plant having an altered phenotype is obtained.

20 3. The method according to claim 1 or 2, wherein said DNA construct is flanked by T-DNA.

4. The method according to claim 3, wherein said plant is a tomato plant.

25 5. A method for modifying the genotype of a plant to impart a desired characteristic to fruit as distinct from other plant tissue, said method comprising:

transforming under genomic integration conditions, a host
30 plant cell with a DNA construct comprising in the 5' to 3' direction of transcription, a transcriptional initiation region from a gene, wherein transcription of said gene is preferentially regulated in a plant fruit tissue, a DNA sequence of interest other than the native coding sequence of said gene, and a transcriptional termination
35 region, whereby said DNA construct becomes integrated into the genome of said plant cell;

regenerating a plant from said transformed host cell; and growing said plant to produce fruit having a modified genotype.

40 6. The method according to claim 5, wherein said DNA construct is flanked by T-DNA.

7. The method according to claim 5, wherein said DNA sequence of interest encodes an enzyme.

8. The method according to claim 5, wherein said DNA
45 sequence of interest is an antisense sequence.

9. A method for modifying transcription in fruit tissue as distinct from other plant tissue, said method comprising:

50 growing a plant capable of developing fruit tissue under conditions to produce fruit, wherein said plant comprises cells containing a DNA construct integrated into their genome, said DNA construct comprising, in the 5' to 3' direction of transcription, a fruit-specific transcriptional initiation region, a DNA sequence of interest other than the coding sequence native to said transcriptional initiation region, and a transcriptional termination
55 region, whereby said DNA sequence of interest is transcribed under transcriptional control of said fruit-specific transcription initiation region.

60 10. The method according to claim 9, wherein said DNA sequence of interest is an antisense sequence.

11. The method according to claim 9, wherein said transcriptional initiation region further comprises a translational initiation region and said DNA sequence of interest is an open reading frame encoding an amino acid sequence.

65 12. A method to selectively express a heterologous DNA sequence of interest in fruit tissue as distinct from other plant tissue, said method comprising:

growing a plant capable of developing fruit tissue under conditions to produce fruit, wherein said plant comprises cells having a genomically integrated DNA construct comprising, as operably linked components in the 5' to 3' direction of transcription, a fruit-specific transcriptional initiation region and a translational initiation region, a DNA sequence of interest other than the coding sequence native to said transcriptional initiation region, a transcriptional termination region downstream of said DNA sequence of interest, whereby said DNA sequence of interest is expressed under control of said fruit-specific transcriptional and translational initiation region. 10

13. The method according to claim 2, wherein said transcriptional initiation region further comprises a transla-

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14. The method according to claim 1 or 2 wherein said DNA sequence of interest encodes an enzyme.

16. The method according to claim 15 wherein said gene is transcribed at or shortly after anthesis.

18. The method according to claim 1 or 2 wherein said DNA sequence of interest is an antisense sequence.

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19. A plant part having an altered phenotype as a result of transcription of a DNA construct comprising as operably linked components in the direction of transcription, a promoter region obtainable from a gene, wherein transcription of said gene is preferentially regulated in a plant tissue selected from the group consisting of embryonic seed tissue, chloroplast containing tissue and fruit tissue; a DNA sequence of interest other than the native coding sequence of said gene which provides for modulation of expression of endogenous products; and a transcription termination region, wherein said components are functional in said plant tissue, whereby said plant part having an altered phenotype is produced.

20. The plant part according to Claim 19, wherein said plant part is from a plant selected from the group consisting of a tomato plant, a soybean plant, a rapeseed plant and a safflower plant.

21. A DNA construct comprising as operably linked components in the direction of transcription, a promoter region obtainable from a gene, wherein transcription of said gene is preferentially regulated in a plant tissue selected from the group consisting of embryonic seed tissue, chloroplast containing tissue, and fruit tissue; a DNA sequence of interest other than the native coding sequence of said gene which provides for modulation of expression of endogenous products; and a transcription termination region, wherein said components are functional in a plant cell.

22. A DNA construct comprising as operably linked components in the direction of transcription, a promoter region obtainable from a gene, wherein transcription of said gene is preferentially regulated in a plant tissue selected from the group consisting of embryonic seed tissue, chloroplast containing tissue and fruit tissue; a DNA sequence of interest from a gene which is native to a plant host or a mutant of a gene which is native to a plant host; and a transcription termination region, wherein said components are functional in said plant host.

23. The DNA construct of Claim 21 or 22, wherein said DNA sequence of interest is an antisense sequence.

24. The DNA construct of Claim 21 or 22, wherein said DNA construct is flanked by T-DNA.

25. A plant cell having an altered phenotype as a result of expression of a DNA construct according to Claim 21 or 22.

26. A plant comprising plant cells comprising a DNA construct according to Claim 21 or 22.

27. The plant according to Claim 26, wherein said plant is dicotyledonous.

28. The plant according to Claim 27, wherein said plant is a legume.

29. The plant according to Claim 27, wherein said plant is selected from the group consisting of tomato, soybean, rapeseed and safflower.

30. A plant cell having integrated into its genome a DNA construct comprising as operably linked components in the direction of transcription, a promoter region obtainable from a gene, wherein transcription of said gene is light-regulated in a plant chloroplast containing tissue; a DNA sequence of interest other than the native coding sequence of said gene and native to a plant host; and a transcription termination region, wherein said components are functional in a plant cell.

31. The plant cell according to Claim 30, wherein said DNA sequence of interest is in the antisense orientation.

32. The plant cell according to Claim 30, wherein said promoter region is an SSU promoter.

33. A DNA construct comprising as operably linked components in the direction of transcription, a promoter region obtainable from a gene, wherein transcription of said gene is light-regulated in a plant chloroplast containing tissue; a DNA sequence of interest other than the native coding sequence of said gene which provides for modulation of expression of endogenous products; and a transcription termination region, wherein said components are functional in a plant cell.

34. The DNA construct comprising as operably linked components in the direction of transcription, a promoter region obtainable from a gene, wherein transcription of said gene is light-regulated in a plant chloroplast containing tissue, a DNA sequence of interest which provides for at least one of increased capability of protein storage, improved nutrient source, enhanced response to light, enhanced dehydration resistance, enhanced herbicide resistance, and enhanced resistance to viruses, insects and fungi.

35. The DNA construct according to Claim 34, wherein said DNA sequence of interest is a mutated *aroA* gene.

36. The DNA construct according to Claim 33, wherein said DNA sequence of interest is in the antisense orientation.

37. The DNA construct according to Claim 33, wherein said promoter region is an SSU promoter.

38. The DNA construct according to Claim 33, wherein said DNA construct is flanked by T-DNA.

39. A plant cell having an altered phenotype as a result of expression of a DNA construct according to Claim 33.

40. A plant comprising cells comprising a DNA construct according to Claim 33.

41. The plant according to Claim 40, wherein said plant is dicotyledonous.

42. The plant according to Claim 41, wherein said plant is selected from the group consisting of tomato, soybean, rapeseed and safflower.

43. A plant part having an altered phenotype as a result of expression of a DNA construct according to Claim 33.

44. The plant part according to Claim 43, wherein said plant part is a leaf or a fruit.

45. A plant cell having integrated into its genome a DNA construct comprising as operably linked components in the direction of transcription, a promoter region obtainable from a gene, wherein transcription of said gene is preferentially regulated in fruit tissue; a DNA sequence of interest other than the native coding sequence of said gene; and a transcription termination region, wherein said components are functional in a plant cell.

46. The plant cell according to Claim 45, wherein said promoter region is selected from a 2A11 gene.

47. The plant cell according to Claim 45, wherein said DNA sequence of interest is in the antisense orientation.

49. A DNA construct comprising as operably linked components in the direction of transcription, a promoter region obtainable from a gene, wherein transcription of said gene is preferentially regulated in fruit tissue; a DNA sequence of interest other than the native coding sequence of said gene; and a transcription termination region, wherein said components are functional in a plant cell.

51. The DNA construct according to Claim 49, wherein said DNA sequence of interest provides for a modified response to stress.

52. The DNA construct according to Claim 51, wherein said DNA sequence of interest is a mutated *aroA* gene.

53. The DNA construct according to Claim 49, wherein said DNA sequence of interest is in the antisense orientation.

54. The DNA construct according to Claim 49, wherein said DNA sequence of interest encodes for a protein selected from the group consisting of sucrose synthase, polygalacturonase, and invertase.

55. The DNA construct according to Claim 49, wherein said promoter region is from a 2A11 gene.

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A plant having a regulatable phenotype comprising as integrated into its genome a construct according to Claim 21, 33 or 49.

A plant with an altered phenotype in a plant tissue of interest comprising as integrated into its genome a DNA construct according to Claim 21, 33 or 49.

A plant with a modified genotype comprising as integrated into its genome a construct according to Claim 21, 33 or 49.

~~64. A plant with a modified genotype comprising as integrated into its genome a DNA construct according to Claim 21, 33 or 49.~~

65. A method for obtaining a plant having a regulatable phenotype, said method comprising:

transforming a host plant cell with a DNA construct under genomic integration conditions, wherein said construct comprises as operably linked components in the direction of transcription, a promoter region obtainable from a gene, wherein transcription of said gene is preferentially associated with a specific stage of plant growth; a DNA sequence of interest other than the native coding sequence of said gene, and a transcription termination region, wherein said components are functional in a plant cell,

whereby said DNA construct becomes integrated into a genome of said plant cell;

regenerating a plant from said transformed plant cell, and

growing said plant under conditions whereby said DNA sequence of interest is expressed and a plant having said regulatable phenotype is obtained.

66. A method for altering the phenotype of a plant tissue of interest as distinct from other plant tissue, said method comprising:

growing a plant, wherein said plant comprises cells containing a DNA construct integrated into their genome, said DNA construct comprising, in the 5' to 3' direction of transcription, a transcriptional initiation region from a gene, wherein transcription of said gene is preferentially associated with a specific stage of plant growth, a DNA sequence of interest other than the coding sequence native to said transcriptional initiation region and a transcriptional termination region, whereby said DNA sequence of interest is transcribed under transcriptional control of said transcriptional initiation region and a plant having an altered phenotype is obtained.

67. The method according to claim 65 or 66, wherein said DNA construct is flanked by T-DNA.

68. The method according to claim 67, wherein said plant is a tomato plant, a soybean plant, a rapeseed plant or a safflower plant.

69. A method for modifying the genotype of a plant to impart a desired characteristic to a plant tissue of interest as distinct from other plant tissue, said method comprising:

transforming under genomic integration conditions, a host plant cell with a DNA construct comprising in the 5' to 3' direction of transcription, a transcriptional initiation region from a gene, wherein transcription of said gene is preferentially associated with a specific stage of plant growth, a DNA sequence of interest other than the native coding sequence of said gene, and a transcriptional termination region, whereby said DNA construct becomes integrated into the genome of said plant cell;

regenerating a plant from said transformed host cell; and

growing said plant to produce a plant tissue of interest having a modified genotype.

70. The method according to claim 69, wherein said DNA construct is flanked by T-DNA.

71. The method according to claim 69, wherein said DNA sequence of interest encodes an enzyme.

72. The method according to claim 69, wherein said DNA sequence of interest is an antisense sequence.

73. A method for modifying transcription in plant tissue of interest as distinct from other plant tissue, said method comprising:

growing a plant capable of developing a plant tissue of interest under conditions to produce said plant tissue of interest, wherein said plant comprises cells containing a DNA construct integrated into their genome, said DNA construct comprising, in the 5'

to 3' direction of transcription, a transcriptional initiation region specifically regulated during a particular stage of plant growth, a DNA sequence of interest other than the coding sequence native to said transcriptional initiation region, and a transcriptional termination region, whereby said DNA sequence of interest is transcribed under transcriptional control of said transcription initiation region specifically regulated in said plant tissue of interest.

74. The method according to claim 73, wherein said DNA sequence of interest is an antisense sequence.

75. The method according to claim 73, wherein said transcriptional initiation region further comprises a translational initiation region and said DNA sequence of interest is an open reading frame encoding an amino acid sequence.

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76. A method to selectively express a heterologous DNA sequence of interest in a plant tissue of interest as distinct from other plant tissue, said method comprising: growing a plant capable of developing a plant tissue of interest under conditions to produce said plant tissue of interest, wherein said plant comprises cells having a genomically integrated DNA construct comprising, as operably linked components in the 5' to 3' direction of transcription, a transcriptional initiation region specifically regulated during a particular stage of plant growth and a translational initiation region, a DNA sequence of interest other than the coding sequence native to said transcriptional initiation region, a transcriptional termination region downstream of said DNA sequence of interest, whereby said DNA sequence of interest is expressed under control of said transcriptional and translational initiation region specifically regulated in said plant tissue of interest.

77. The method according to claim 66, wherein said transcriptional initiation region further comprises a translational initiation region and said DNA sequence of interest is an open reading frame encoding an amino acid sequence.

78. The method according to claim 65 or 66 wherein said DNA sequence of interest encodes an enzyme.

79. The method according to claim 65 or 66 wherein said gene is transcribed at or shortly after anthesis.

80. The method according to claim 65 or 66 wherein said DNA sequence of interest is an antisense sequence.

81. A method for obtaining a plant having a regulatable phenotype, said method comprising:

transforming a host plant cell with a DNA construct under genomic integration conditions, wherein said construct comprises as operably linked components in the direction of transcription, a promoter region obtainable from a gene, wherein transcription of said gene is preferentially regulated in a plant tissue selected from the group consisting of chloroplast containing tissue, embryonic seed tissue and fruit tissue; a DNA sequence of interest other than the native coding sequence of said gene which provides for modulation of expression of endogenous products, and a transcription termination region, wherein said components are functional in a plant cell,

whereby said DNA construct becomes integrated into a genome of said plant cell;

regenerating a plant from said transformed plant cell, and

growing said plant under conditions whereby said DNA sequence of interest is expressed and a plant having said regulatable phenotype is obtained.

82. A method for altering the phenotype of a plant tissue of interest as distinct from other plant tissue, said method comprising:

growing a plant, wherein said plant comprises cells containing a DNA construct integrated into their genome, said DNA construct comprising, in the 5' to 3' direction

of transcription, a transcriptional initiation region from a gene, wherein transcription of said gene is preferentially regulated in a plant tissue selected from the group consisting of chloroplast containing tissue, embryonic seed tissue and fruit tissue, a DNA sequence of interest other than the coding sequence native to said transcriptional initiation region which provides for modulation of expression of endogenous products, and a transcriptional termination region, whereby said DNA sequence of interest is transcribed under transcriptional control of said transcriptional initiation region and a plant having an altered phenotype is obtained.

83. The method according to claim 81 or 82, wherein said DNA construct is flanked by T-DNA.

84. The method according to claim 83, wherein said plant is a tomato plant, a soybean plant, a rapeseed plant or a safflower plant.

85. A method for modifying the genotype of a plant to impart a desired characteristic to a plant tissue of interest as distinct from other plant tissue, said method comprising:

transforming under genomic integration conditions, a host plant cell with a DNA construct comprising in the 5' to 3' direction of transcription, a transcriptional initiation region from a gene, wherein transcription of said gene is preferentially regulated in a plant tissue selected from the group consisting of chloroplast containing tissue, embryonic seed tissue and fruit tissue, a DNA sequence of interest other than the native coding sequence of said gene which provides for modulation of expression of endogenous products, and a transcriptional termination region, whereby said DNA construct becomes integrated into the genome of said plant cell;

regenerating a plant from said transformed host cell; and

growing said plant to produce a plant tissue of interest having a modified genotype.

86. The method according to claim 85, wherein said DNA construct is flanked by T-DNA.

87. The method according to claim 85, wherein said DNA sequence of interest encodes an enzyme.

88. The method according to claim 85, wherein said DNA sequence of interest is an antisense sequence.

89. A method for modifying transcription in plant tissue of interest as distinct from other plant tissue, said method comprising:

growing a plant capable of developing a plant tissue of interest under conditions to produce said plant tissue of interest, wherein said plant comprises cells containing a DNA construct integrated into their genome, said DNA construct comprising, in the 5' to 3' direction of transcription, a transcriptional initiation region specifically regulated in a plant tissue selected from the group consisting of chloroplast containing tissue, embryonic seed tissue and fruit tissue, a DNA sequence of interest other than the coding sequence native to said transcriptional initiation region which provides for modulation of expression of endogenous products, and a transcriptional termination region, whereby said DNA sequence of interest is transcribed under transcriptional control of said transcription initiation region specifically regulated in said plant tissue of interest.

90. The method according to claim 89, wherein said DNA sequence of interest is an antisense sequence.

91. The method according to claim 89, wherein said transcriptional initiation region further comprises a translational initiation region and said DNA sequence of interest is an open reading frame encoding an amino acid sequence.

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92. A method to selectively express a heterologous DNA sequence of interest in a plant tissue of interest as distinct from other plant tissue, said method comprising:

growing a plant capable of developing a plant tissue of interest under conditions to produce said plant tissue of interest, wherein said plant comprises cells having a genomically integrated DNA construct comprising, as operably linked components in the 5' to 3' direction of transcription, a transcriptional initiation region specifically regulated in a plant tissue selected from the group consisting of chloroplast containing tissue, embryonic seed tissue and fruit tissue, and a translational initiation region, a DNA sequence of interest other than the coding sequence native to said transcriptional initiation region which provides for modulation of expression of endogenous products, a transcriptional termination region downstream of said DNA sequence of interest, whereby said DNA sequence of interest is expressed under control of said transcriptional and translational initiation region specifically regulated in said plant tissue of interest.

93. The method according to claim 82, wherein said transcriptional initiation region further comprises a translational initiation region and said DNA sequence of interest is an open reading frame encoding an amino acid sequence.

94. The method according to claim 81 or 82 wherein said DNA sequence of interest encodes an enzyme.

95. The method according to claim 81 or 82 wherein said gene is transcribed at or shortly after anthesis.

96. The method according to claim 81 or 82 wherein said DNA sequence of interest is an antisense sequence.

97. A method for obtaining a plant having a regulatable phenotype, said method comprising:

transforming a host plant cell with a DNA construct under genomic integration conditions, wherein said construct comprises as operably linked components in the direction of transcription, a promoter region obtainable from a gene, wherein transcription of said gene is preferentially regulated in a plant tissue selected from the group consisting of chloroplast containing tissue, embryonic seed tissue and fruit tissue; a DNA sequence of interest other than the native coding sequence of said gene which is from a gene native to a plant host or a mutant of a gene which is native to a plant host, and a transcription termination region, wherein said components are functional in a plant cell,

whereby said DNA construct becomes integrated into a genome of said plant cell;

regenerating a plant from said transformed plant cell, and

growing said plant under conditions whereby said DNA sequence of interest is expressed and a plant having said regulatable phenotype is obtained.

98. A method for altering the phenotype of a plant tissue of interest as distinct from other plant tissue, said method comprising:

growing a plant, wherein said plant comprises cells containing a DNA construct integrated into their genome, said DNA construct comprising, in the 5' to 3' direction of transcription, a transcriptional initiation region from a gene, wherein transcription of said gene is preferentially regulated in a plant tissue selected from the group consisting of chloroplast containing tissue, embryonic seed tissue and fruit tissue, a DNA sequence of interest other than the coding sequence native to said transcriptional initiation region which is from a gene native to a plant host or a mutant of a gene which is native to a plant host, and a transcriptional termination region, whereby said DNA sequence of interest is transcribed under transcriptional control of said transcriptional initiation region and a plant having an altered phenotype is obtained.

99. The method according to claim 97 or 98, wherein said DNA construct is flanked by T-DNA.

100. The method according to claim 99, wherein said plant is a tomato plant, a soybean plant, a rapeseed plant or a safflower plant.

101. A method for modifying the genotype of a plant to impart a desired characteristic to a plant tissue of interest as distinct from other plant tissue, said method comprising:

transforming under genomic integration conditions, a host plant cell with a DNA construct comprising in the 5' to 3' direction of transcription, a transcriptional initiation region from a gene, wherein transcription of said gene is preferentially regulated in a plant tissue selected from the group consisting of chloroplast containing tissue, embryonic seed tissue and fruit tissue, a DNA sequence of interest other than the native coding sequence of said gene which is from a gene native to a plant host or a mutant of a gene which is native to a plant host, and a transcriptional termination region, whereby said DNA construct becomes integrated into the genome of said plant cell;

regenerating a plant from said transformed host cell; and

growing said plant to produce a plant tissue of interest having a modified genotype.

102. The method according to claim 101, wherein said DNA construct is flanked by T-DNA.

103. The method according to claim 101, wherein said DNA sequence of interest encodes an enzyme.

104. The method according to claim 101, wherein said DNA sequence of interest is an antisense sequence.

105. A method for modifying transcription in plant tissue of interest as distinct from other plant tissue, said method comprising:

growing a plant capable of developing a plant tissue of interest under conditions to produce said plant tissue of interest, wherein said plant comprises cells containing a DNA construct integrated into their genome, said DNA construct comprising, in the 5' to 3' direction of transcription, a transcriptional initiation region specifically regulated in a plant tissue selected from the group consisting of chloroplast containing tissue, embryonic seed tissue and fruit tissue, a DNA sequence of interest other than the coding sequence native to said transcriptional initiation region which is from a gene native to a plant host or a mutant of a gene which is native to a plant host, and a transcriptional termination region, whereby said DNA sequence of interest is transcribed under transcriptional control of said transcription initiation region specifically regulated in said plant tissue of interest.

106. The method according to claim 105, wherein said DNA sequence of interest is an antisense sequence.

107. The method according to claim 105, wherein said transcriptional initiation region further comprises a translational initiation region and said DNA sequence of interest is an open reading frame encoding an amino acid sequence.

108. A method to selectively express a heterologous DNA sequence of interest in a plant tissue of interest as distinct from other plant tissue, said method comprising:

growing a plant capable of developing a plant tissue of interest under conditions to produce said plant tissue of interest, wherein said plant comprises cells having a genomically integrated DNA construct comprising, as operably linked components in the 5' to 3' direction of transcription, a transcriptional initiation region specifically regulated in a plant tissue selected from the group consisting of chloroplast containing tissue, embryonic seed tissue and fruit tissue, and a translational initiation region, a DNA sequence of interest other than the coding sequence native to said transcriptional

initiation region which is from a gene native to a plant host or a mutant of a gene which is native to a plant host, a transcriptional termination region downstream of said DNA sequence of interest, whereby said DNA sequence of interest is expressed under control of said transcriptional and translational initiation region specifically regulated in said plant tissue of interest.

109. The method according to claim 100, wherein said transcriptional initiation region further comprises a translational initiation region and said DNA sequence of interest is an open reading frame encoding an amino acid sequence.

110. The method according to claim 97 or 98 wherein said DNA sequence of interest encodes an enzyme.

111. The method according to claim 97 or 98 wherein said gene is transcribed at or shortly after anthesis.

112. The method according to claim 97 or 98 wherein said DNA sequence of interest is an antisense sequence.

113. A method for obtaining a plant having a regulatable phenotype, said method comprising:

transforming a host plant cell with a DNA construct under genomic integration conditions, wherein said construct comprises as operably linked components in the direction of transcription, a promoter region obtainable from a gene, wherein transcription of said gene is preferentially regulated in a plant tissue selected from the group consisting of chloroplast containing tissue, embryonic seed tissue and fruit tissue; a DNA sequence of interest other than the native coding sequence of said gene which provides for at least one of increased capability of protein storage, improved nutrient source, enhanced response to light, enhanced dehydration resistance, enhanced

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herbicide resistance, and enhanced resistance to viruses, insects and fungi; and a transcription termination region, wherein said components are functional in a plant cell, whereby said DNA construct becomes integrated into a genome of said plant cell;
regenerating a plant from said transformed plant cell, and
growing said plant under conditions whereby said DNA sequence of interest is expressed and a plant having said regulatable phenotype is obtained.

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114. A method for altering the phenotype of a plant tissue of interest as distinct from other plant tissue, said method comprising:
growing a plant, wherein said plant comprises cells containing a DNA construct integrated into their genome, said DNA construct comprising, in the 5' to 3' direction of transcription, a transcriptional initiation region from a gene, wherein transcription of said gene is preferentially regulated in a plant tissue selected from the group consisting of chloroplast containing tissue, embryonic seed tissue and fruit tissue, a DNA sequence of interest other than the coding sequence native to said transcriptional initiation region which provides for at least one of increased capability of protein storage, improved nutrient source, enhanced response to light, enhanced dehydration resistance, enhanced herbicide resistance, and enhanced resistance to viruses, insects and fungi; and a transcriptional termination region, whereby said DNA sequence of interest is transcribed under transcriptional control of said transcriptional initiation region and a plant having an altered phenotype is obtained.

115. The method according to claim 113 or 114, wherein said DNA construct is flanked by T-DNA.

116. The method according to claim 115, wherein said plant is a tomato plant, a soybean plant, a rapeseed plant or a safflower plant.

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117. A method for modifying the genotype of a plant to impart a desired characteristic to a plant tissue of interest as distinct from other plant tissue, said method comprising:

transforming under genomic integration conditions, a host plant cell with a DNA construct comprising in the 5' to 3' direction of transcription, a transcriptional initiation region from a gene, wherein transcription of said gene is preferentially regulated in a plant tissue selected from the group consisting of chloroplast containing tissue, embryonic seed tissue and fruit tissue, a DNA sequence of interest other than the native coding sequence of said gene which provides for at least one of increased capability of protein storage, improved nutrient source, enhanced response to light, enhanced dehydration resistance, enhanced herbicide resistance, and enhanced resistance to viruses, insects and fungi and a transcriptional termination region, whereby said DNA construct becomes integrated into the genome of said plant cell;

regenerating a plant from said transformed host cell; and

growing said plant to produce a plant tissue of interest having a modified genotype.

118. The method according to claim 117, wherein said DNA construct is flanked by T-DNA.

119. The method according to claim 117, wherein said DNA sequence of interest encodes an enzyme.

120. The method according to claim 117, wherein said DNA sequence of interest is an antisense sequence.

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121. A method for modifying transcription in plant tissue of interest as distinct from other plant tissue, said method comprising:

growing a plant capable of developing a plant tissue of interest under conditions to produce said plant tissue of interest, wherein said plant comprises cells containing a

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DNA construct integrated into their genome, said DNA construct comprising, in the 5' to 3' direction of transcription, a transcriptional initiation region specifically regulated in a plant tissue selected from the group consisting of chloroplast containing tissue, embryonic seed tissue and fruit tissue, a DNA sequence of interest other than the coding sequence native to said transcriptional initiation region which provides for at least one of increased capability of protein storage, improved nutrient source, enhanced response to light, enhanced dehydration resistance, enhanced herbicide resistance, and enhanced resistance to viruses, insects and fungi; and a transcriptional termination region, whereby said DNA sequence of interest is transcribed under transcriptional control of said transcription initiation region specifically regulated in said plant tissue of interest.

122. The method according to claim 121, wherein said DNA sequence of interest is an antisense sequence.

123. The method according to claim 121, wherein said transcriptional initiation region further comprises a translational initiation region and said DNA sequence of interest is an open reading frame encoding an amino acid sequence.

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124. A method to selectively express a heterologous DNA sequence of interest in a plant tissue of interest as distinct from other plant tissue, said method comprising: growing a plant capable of developing a plant tissue of interest under conditions to produce said plant tissue of interest, wherein said plant comprises cells having a genomically integrated DNA construct comprising, as operably linked components in the 5' to 3' direction of transcription, a transcriptional initiation region specifically regulated in a plant tissue selected from the group consisting of chloroplast containing tissue, embryonic seed tissue and fruit tissue, and a translational initiation region, a DNA sequence of interest other than the coding sequence native to said transcriptional initiation region which provides for at least one of increased capability of protein storage, improved nutrient source, enhanced response to light, enhanced dehydration

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resistance, enhanced herbicide resistance, and enhanced resistance to viruses, insects and fungi; a transcriptional termination region downstream of said DNA sequence of interest, whereby said DNA sequence of interest is expressed under control of said transcriptional and translational initiation region specifically regulated in said plant tissue of interest.

125. The method according to claim 114, wherein said transcriptional initiation region further comprises a translational initiation region and said DNA sequence of interest is an open reading frame encoding an amino acid sequence.

126. The method according to claim 113 or 114 wherein said DNA sequence of interest encodes an enzyme.

127. The method according to claim 113 or 114 wherein said gene is transcribed at or shortly after anthesis.

128. The method according to claim 113 or 114 wherein said DNA sequence of interest is an antisense sequence.

129. A method for obtaining a plant having a regulatable phenotype, said method comprising:

transforming a host plant cell with a DNA construct under genomic integration conditions, wherein said construct comprises as operably linked components in the direction of transcription, a promoter region obtainable from a gene, wherein transcription of said gene is preferentially regulated in a plant tissue of interest; a DNA sequence of interest other than the native coding sequence of said gene that is not phaseolin; and a transcription termination region, wherein said components are functional in a plant cell,

whereby said DNA construct becomes integrated into a genome of said plant cell;

regenerating a plant from said transformed plant cell, and
growing said plant under conditions whereby said DNA sequence of interest is
expressed and a plant having said regulatable phenotype is obtained.

130. A method for altering the phenotype of a plant tissue of interest as
distinct from other plant tissue, said method comprising:

growing a plant, wherein said plant comprises cells containing a DNA construct
integrated into their genome, said DNA construct comprising, in the 5' to 3' direction
of transcription, a transcriptional initiation region from a gene, wherein transcription of
said gene is preferentially regulated in a plant tissue of interest, a DNA sequence of
interest other than the coding sequence native to said transcriptional initiation region
that is not phaseolin; and a transcriptional termination region, whereby said DNA
sequence of interest is transcribed under transcriptional control of said transcriptional
initiation region and a plant having an altered phenotype is obtained.